



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160722

TO: Mark Shibuya
Location: REM-2A10&2C18
Art Unit: 1639
Monday, August 01, 2005

Case Serial Number: 09/667237

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Shibuya,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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160722

From: Shibuya, Mark
Sent: Wednesday, July 27, 2005 2:30 PM
To: STIC-Biotech/ChemLib
Subject: Search req. for SEQ NO:12 of 09/667,237.

Please search SEQ NO:12 of 09/667,237.

This case is before the first action on the merits.

Mark Shibuya
Art Unit 1639, Remsen 2a10, ext: 2-0806

CRPE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 8/17/05
Date Completed: 8/17/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 1 AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: SP1
WWW/Internet: _____
Other(Specify): _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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RESULT 6
BX470087/c
LOCUS      BX470087      218404 bp      DNA      linear      VRT 26-FEB-2004
DEFINITION Zebrafish DNA sequence from clone CH211-202A10 in linkage group 3,
complete sequence.
ACCESSION  BX470087
VERSION     BX470087.8  GI:43823873
KEYWORDS    HTG.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 218404)
AUTHORS     Pelan,S.
TITLE       Direct Submission
JOURNAL
COMMENT     Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
            On Feb 26, 2004 this sequence version replaced gi:42820884.
            ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Web site: http://www.sanger.ac.uk
            Contact: zf1sh-help@sanger.ac.uk
            -----
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems; such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information
            on the WormPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep/
            Zebrafish pUC subclones occasionally display inconsistency over the
            length of mononucleotide A/T runs and conserved TA repeats. Where
            this is found the longest good quality representation will be
            submitted.
            Repeat names beginning 'Dr' were identified by the Recon repeat
            discovery system (Zhirong Bao and Sean Eddy, submitted), and those
            beginning 'dr' were identified by Rick Waterman (Stephen Johnson
            lab, WashU). For further information see
            http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
            CH211-202A10 is from a CHORI-211 BAC library
            VECTOR: pFARBAC2.1.
FEATURES             Location/Qualifiers
     source           1..218404
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="CH211-202A10"
                     /clone_lib="CHORI-211"

ORIGIN
Query Match      79.5%; Score 31; DB 5; Length 218404;
Best Local Similarity 87.2%; Pred. No. 2;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGGCTAGTACTACTGCTGCTGGTGGTACT 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28923 ACTACTACTACTGCTACTAGTACTACTGCTGCTGCTACT 28895

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RESULT 7
AC126150/c
LOCUS      AC126150      241173 bp      DNA      linear      HTG 13-MAY-2003
DEFINITION Rattus norvegicus clone CH230-69L10, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.
ACCESSION  AC126150
VERSION     AC126150.4  GI:30580907
KEYWORDS    HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 241173)
AUTHORS     Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalabechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Bismail,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Caldwell,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorenschwah,L., Louissegh,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahlstedt,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwokeneme,O., Okwuonu,G., Olarunpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu.L.L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Snajds,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Uemami,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
            Direct Submission
            Unpublished
            2 (bases 1 to 241173)
            Worley,K.C.
            Direct Submission
            Submitted (04-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 241173)
            REFERENCE

```

AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT
 On May 13, 2003 this sequence version replaced gi:23268918.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information
 Center project name: GIWC
 Center clone name: CH230-69L10
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 21355 bases at least Q40
 Consensus quality: 219597 bases at least Q30
 Consensus quality: 223913 bases at least Q20
 Estimated insert size: 225595; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES
 source
 1 239825: contig of 239825 bp in length
 2 239826: gap of unknown length
 3 239926: contig of 1248 bp in length.

Location/Qualifiers
 1..241173
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clones="CH230-69L10"
 1..1631
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 31777..33772
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 101829..103618
 /note="wgs contig"
 193630..194760
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 226377..227570
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misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature

ORIGIN
 Query Match 79.5%; Score 31; DB 2; Length 241173;
 Best Local Similarity 87.2%; Pred. No. 1.9;
 Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACTACTGCTAGTCTAGTACTACTACTGCTGCTAGT 39
 Db 21848 ACTACTGCTAGTCTAGTACTACTGCTGCTACT 21810

RESULT 8
LOCUS BV090840
DEFINITION 402 bp DNA linear STS 15-OCT-2003
 RPAMSEQ0002739 Roche Palo Alto Mus musculus STS genomic, sequence
 tagged site.
ACCESSION BV090840
VERSION BV090840.1 GI:37668319
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 402)
AUTHORS Usuka, J., Liao, G., Cheng, J., Nguyen, A., Bach, C., Puech, A.,
 McPherson, J.D., Foerzler, D. and Peltz, G.
TITLE Mus musculus SNPs
JOURNAL Unpublished (2003)
COMMENT Contact: Jonathan Usuka
 Roche Palo Alto Genetics and Genomics Department
 Roche Palo Alto
 3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA 94024, USA
 Tel: 6508555807
 Email: Jonathan.Usuka@roche.com
 Primer A: No primer submitted
 Primer B: No primer submitted.

FEATURES
 source
 1..402
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /map="7-144325-144544-AC087063.20.1.241381"
 /clone_lib="Roche Palo Alto"
 /note="SNPs developed from assay sequences derived from 15
 different strains of mice (as of October 1, 2003). Those
 strains include A/J, A/HeJ, -129/sv, AKR/J, B10.D2-H2/oshJ,
 BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J, -CAST/Ei, DBA/2J,
 MRL/MpJ, NZB/BinJ, NZW/Lac, SPRET/Ei.-"
 <1..>402

STIS
ORIGIN
 Query Match 76.9%; Score 30; DB 11; Length 402;
 Best Local Similarity 86.8%; Pred. No. 6.6;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CTACTGCTAGTCTAGTACTACTGCTGCTGCTAGT 39
 Db 169 CTCTGCTGCTGCTAGTATTCTCTGCTGCTAGT 206

RESULT 9
LOCUS AF329581
DEFINITION 410 bp DNA linear INV 15-MAR-2001
 Plasmodium falciparum genotype 3 from Solomon Islands merozoite
 surface protein 2 gene, partial cds.
ACCESSION AF329581
VERSION AF329581.1 GI:133455560
KEYWORDS .
SOURCE Plasmodium falciparum (malaria parasite P. falciparum)
ORGANISM Plasmodium falciparum
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 410)
AUTHORS Eisen, D.P., Cloonan, N., Baddeley, A., Eri, R. and Saul, A.
TITLE Antigenic drift and immune selection acting on merozoite surface
 protein 1-19 and merozoite surface protein 2 in independent field
 isolates of Plasmodium falciparum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 410)
AUTHORS Eisen, D.P., Cloonan, N., Baddeley, A., Eri, R. and Saul, A.
TITLE Direct Submission
JOURNAL Infectious Diseases, Royal Brisbane
 Hospital, Herston Rd., Herston, QLD 4029, Australia

[illegible]

KEYWORDS

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Morris,D.W., Morris,D.W. and Malandro,M.S.

Novel therapeutic targets in cancer

Patent: WO 2004074320-A 313 02-SEP-2004;

Sagres Discovery, Inc. (US)

FEATURES

source Location/Qualifiers

1. 109453

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

ORIGIN

Query Match 76.9%; Score 30; DB 6; Length 109453;
 Best Local Similarity 86.8%; Pred. No. 4.5;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CTACTGCTACTGGTGCTAGTACTGCTGCTGCTACT 39

Db 22948 CTGCTGCTGCTGGTGCTAGTACTGCTGCTGCTACT 22985

RESULT 13

AC117361/c

LOCUS AC117361 203739 bp DNA linear HTG 15-NOV-2002
 DEFINITION Rattus norvegicus clone CH230-228G24, WORKING DRAFT SEQUENCE, 4
 unorderded pieces.

ACCESSION

VERSION AC117361.6 GI:25009654

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

Rattus norvegicus (Norway rat)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

1 (bases 1 to 203739)

Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angulano,D.,
 Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Blawalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
 Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
 Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
 Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
 Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
 Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
 Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
 Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
 Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
 Lorensuhewa,L., Lounsged,H., Lozado,R.J., Lu,X., Ma,J.,
 Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
 Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
 Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
 Morgan,M., Morris,K., Morris,S., Munidasa M., Murphy,M., Nair,L.,
 Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
 Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
 Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,

Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
 Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
 Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
 Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
 Shetty,J., Shwartzbeyn,A., Sisson,J., Sitter,C.D., Smajs,D.,
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
 Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
 Valas,R., Vera,V., Villasaana,D., Waldron,L., Walker,B., Wang,J.,
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
 Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstein,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 203739)

Worley,K.C.

Direct Submission

Submitted (10-APR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 203739)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23194821.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature

table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GUVB

Center clone name: CH230-228G24

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 189683 bases at least Q40

Consensus quality: 192245 bases at least Q30

Consensus quality: 193914 bases at least Q20

Estimated insert size: 195808; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 111630: contig of 111630 bp in length

* 111631 111730: gap of unknown length

* 111731 201448: contig of 89718 bp in length

* 201449 201548: gap of unknown length

```

* 201549 202550: contig of 1002 bp in length
* 202551 202650: gap of unknown length
* 202651 203739: contig of 1089 bp in length.
FEATURES             source
  1. 203739
     /organism="Rattus norvegicus"
     /mol_type="genomic DNA"
     /db_xref="taxon:10116"
     /clone="CH230-228G24"
misc_feature         109021..111630
                     /note="wgs contig"
misc_feature         171475..172939
                     /note="wgs contig"
ORIGIN
Query Match          76.9%; Score 30; DB 2; Length 203739;
Best Local Similarity 86.8%; Pred. No. 4.3;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy  2 CTACTGCTACTGCTAGTACTACTGCTGCTGCTAGT 39
      ||||| ||||| ||||| ||||| ||||| |||||
Db  146670 CTACTACTGCTGCTACTACTACTGCTGCTGCTACT 146633

RESULT 14
AC087063
LOCUS      AC087063            241381 bp    DNA    linear    ROD 18-SEP-2003
DEFINITION Mus musculus clone rp23-20047 map 7 strain C57BL/6J, complete
           sequence.
ACCESSION  AC087063
VERSION    AC087063.20 GI:25046376
KEYWORDS   HTG.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Mus musculus BAC Clone rp23-20047
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (02-DEC-2000) Department Of Chemistry And Biochemistry,
           The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
           OK 73019, USA
REFERENCE  3 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (14-JUL-2002) Department Of Chemistry And Biochemistry,
           The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
           OK 73019, USA
REFERENCE  4 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (16-JUL-2002) Department Of Chemistry And Biochemistry,
           The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
           OK 73019, USA
REFERENCE  5 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (01-SEP-2002) Department Of Chemistry And Biochemistry,
           The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
           OK 73019, USA
REFERENCE  6 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (21-SEP-2002) Department Of Chemistry And Biochemistry,
           The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
           OK 73019, USA
REFERENCE  7 (bases 1 to 241381)
AUTHORS   Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE     Direct Submission

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JOURNAL      Submitted (16-NOV-2002) Department Of Chemistry And Biochemistry,
              The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA
REFERENCE    8 (bases 1 to 241381)
AUTHORS     Wu,H., Hu,P., Yang,L., Prescott,A., Delisle,B. and Roe,B.A.
TITLE       Direct Submission
JOURNAL     Submitted (18-SEP-2003) Department Of Chemistry And Biochemistry,
              The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA
COMMENT     On Nov 16, 2002 this sequence version replaced gi:21747519.
           ----- Genome Center
           Center: Department Of Chemistry And Biochemistry
           The University Of Oklahoma
           Center code:UOKNOR
           -----
FEATURES             Location/Qualifiers
  source            1. 241381
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /map="7"
                     /clone="rp23-20047"
                     /clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
ORIGIN
Query Match          76.9%; Score 30; DB 10; Length 241381;
Best Local Similarity 86.8%; Pred. No. 4.3;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy  2 CTACTGCTACTGCTAGTACTACTGCTGCTGCTAGT 39
      ||||| ||||| ||||| ||||| ||||| |||||
Db  144313 CTGCTGCTGCTGGTAGTATTCTGCTGCTAGT 144350

RESULT 15
AC117014
LOCUS      AC117014            255613 bp    DNA    linear    HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-123D20, *** SEQUENCING IN PROGRESS
           ***, 5 unordered pieces.
ACCESSION  AC117014
VERSION    AC117014.4 GI:25013195
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 255613)
AUTHORS   Muzny,D.,Marie., Metzker,M.,Lee., Abramzon,S., Adams,C., Alder,J.,
           Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
           Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
           Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,P.,
           Blawalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
           Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,B.,
           Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
           Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
           Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
           Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
           Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
           Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
           Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
           Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
           Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
           Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guvvara,W.,
           Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
           Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
           Hollins,B., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
           Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
           Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
           Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
           Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,

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CC This invention relates to a library of dual-domain nucleic acid
 CC molecules. The two domains in the molecules are separated and linked by a
 CC linker which is a member of a randomised library of linkers. The linkers
 CC in the library vary in size and nucleotide sequence and consist of a
 CC repeated pattern of degenerate repeated triplet nucleotides. Included in
 CC the invention is a method for the production of the library. The library
 CC is useful for producing dual-domain proteins of interest that have
 CC therapeutic value, e.g., idiotype scFv vaccine for treating B-cell
 CC lymphomas. The present sequence represents a linker oligonucleotide
 CC sequence generated in an example illustrating the invention. The example
 CC concerns the generation of a tumour antigen from a patient that includes
 CC the idiotype of CJ B cell lymphoma

XX
 SQ Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTAGTACTACTGCTAGTCTGCTAGT 39
 |||||
 DB 1 ACTACTGCTACTGCTAGTACTACTGCTAGTCTGCTAGT 39

RESULT 2
 AAS45570
 ID AAS45570 standard; DNA; 39 BP.
 XX
 AC AAS45570;
 DT 18-DEC-2001 (first entry)
 DE B cell lymphoma CJ linker library, linker nucleotide sequence #1.
 XX Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen;
 KW tumour-specific vaccine; tumour; polyclonal immune response;
 KW idiotype-specific anti-lymphoma immune response; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX WO200168682-A1.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028362.
 XX
 PR 10-MAR-2000; 2000US-00522900.
 XX (LARG-) LARGE SCALE BIOLOGY CORP.
 PA (MCCO/) MCCORMICK A A.
 PA (TUSE/) TUSE D.

Reinl SJ, Turpen TH;
 WPI; 2001-596903/67.
 DR P-PSDB; AAU29012.
 XX
 PT Novel polypeptide vaccine produced in plants, useful for inducing an
 PT immune response to a self-antigen on the surface of certain tumor cells.
 XX
 PS Example 2; Page 59; 89pp; English.

XX The invention relates to a novel polypeptide self-antigen (I) useful as a
 CC tumour-specific vaccine in a subject with a tumour or at risk of
 CC developing a tumour. (I) includes an epitope or epitopes unique to, or
 CC over expressed by, cells of the tumour, thereby distinguishing the tumour
 CC from all other tumours of the same or different histological type, or in
 CC the subject or in another member of the subject's species. (I) is
 CC epitopes in their native form. (I) is capable of inducing an immune
 CC response in a mammal, when used as an individual-specific immunogenic
 CC product comprising (I); and as a vaccine composition useful for inducing
 CC a tumour-specific immune response, idiotype-specific anti-lymphoma immune

CC response, a polyclonal immune response to at least one idiotype of a
 CC surface immunoglobulin or a polyclonal immune response to an idiotype.
 CC The vaccine composition is useful for inducing a tumour-specific immune
 CC antibody response in a tumour-bearing subject or a subject who had a
 CC tumour e.g. B-cell lymphoma, and was treated so that no tumour is
 CC clinically or radiographically evident. (I) is useful for inducing a
 CC protective antitumour immune response. (I) can be produced at high
 CC levels, is easy to purify and can be appropriately folded to mimic the
 CC conformation of the native epitopes displayed at the tumour cell surface.
 CC AAS45529-AAS45579 represent B cell lymphoma self antigen vaccine linker
 CC sequences and PCR primers of the invention

XX
 SQ Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTAGTACTACTGCTAGTCTGCTAGT 39
 |||||
 DB 1 ACTACTGCTACTGCTAGTACTACTGCTAGTCTGCTAGT 39

RESULT 3
 ACD40364
 ID ACD40364 standard; DNA; 39 BP.
 XX
 AC ACD40364;
 DT 03-SEP-2003 (first entry)
 DE DNA encoding CJ heavy chain variable region linker #1.
 XX Gene; ds; gene therapy; vaccine; tumour; immunoglobulin V; IgV;
 KW CJ heavy chain; variable region; linker.
 XX
 OS Synthetic.
 XX US2003035807-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 08-FEB-2002; 2002US-00067790.
 XX
 PR 24-SEP-1999; 99US-0155979P.
 PR 10-MAR-2000; 2000US-00522900.
 XX (MCCO/) MCCORMICK A A.
 PA (TUSE/) TUSE D.
 PA (REIN/) REINL S J.
 PA (LIND/) LINDBO J A.
 PA (TURP/) TURPEN T H.

Mccormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
 WPI; 2003-492106/46.
 DR P-PSDB; ABO23260.
 XX
 PT Use of a polypeptide self-antigen as a tumor-specific vaccine.
 XX
 PS Example 2; Page 22; 47pp; English.

XX The invention relates to a polypeptide self-antigen useful as a tumour-
 CC specific vaccine in a subject with a tumour or at risk of developing a
 CC tumour and is encoded at least in part by a nucleic acid in the cells of
 CC the tumour. The polypeptide self antigen is useful for treating or
 CC preventing tumour. The present sequence represents DNA encoding a CJ
 CC heavy chain variable region linker

XX
 SQ Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0015;

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Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTGCTGCTAGT 39
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGCTGCTAGT 39

RESULT 4
ACD06879
ID ACD06879 standard; DNA; 39 BP.
XX AC ACD06879;
XX AC ACD06879;
XX DT 06-AUG-2003 (first entry)
XX DE Immunogenic single chain antibody polypeptide (scfv) linker DNA #1.
XX KW Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine;
XX KW self-antigen; tumour-specific vaccine; B-cell lymphoma-specific vaccine;
XX KW B-cell lymphoma; PCR; primer; ss; single chain antibody polypeptide.
XX OS Homo sapiens.
XX PN US2003044420-A1.
XX PD 06-MAR-2003.
XX PP 08-FEB-2002; 2002US-00067893.
XX PR 24-SEP-1999; 99US-0155979P.
XX PR 10-MAR-2000; 2000US-00522900.
XX PA (MCCO/) MCCORMICK A A.
XX PA (TUSE/) TUSE D.
XX PA (REIN/) REINL S J.
XX PA (LIND/) LINDBO J A.
XX PA (TURP/) TURPEN T H.
XX PI McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
XX WPI; 2003-456552/43.
XX DR Novel polypeptide self-antigen useful as tumor-specific vaccine in
XX PT mammals, is produced in plants and mimics one or more epitopes of antigen
XX PT uniquely expressed by cells of tumor.
XX PS Example 2; Page 21; 47pp; English.
XX CC The invention describes a polypeptide self-antigen (I) useful as a tumour
XX CC -specific vaccine in a subject with a tumour or at risk of developing a
XX CC tumour, encoded by a nucleic acid (NA) in the cells of the tumour,
XX CC including an epitope to, or overexpressed by tumour cells; produced in a
XX CC cell or organism that has been transfected with NA and in a correctly
XX CC folded form; and capable of inducing an immune response in a mammal. (I)
XX CC is useful as a tumour-specific vaccine, especially a B-cell lymphoma-
XX CC specific vaccine. A vaccine is useful for inducing a tumour-specific
XX CC immune antibody response in a tumour-bearing subject, preferably human or
XX CC a subject who had a tumour and was treated so that no tumour is
XX CC clinically or radiographically evident, where the tumour is B-cell
XX CC lymphoma. This sequence represents a primer used to isolate DNA encoding
XX CC tumour associated single chain antibody polypeptides
XX SQ Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTGCTGCTAGT 39
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGCTGCTAGT 39

RESULT 6
ACD45089
ID ACD45089 standard; DNA; 39 BP.
XX AC ACD45089;
XX AC ACD45089;
```

```
RESULT 5
ACD06137
ID ACD06137 standard; DNA; 39 BP.
XX AC ACD06137;
XX AC ACD06137;
XX DT 06-AUG-2003 (first entry)
XX DE Immunogenic single chain antibody polypeptide (scfv) linker DNA #1.
XX KW Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine;
XX KW inducer of immune response; self-antigen; B-cell lymphoma;
XX KW tumour-specific vaccine; single chain antibody polypeptide; linker; ds.
XX OS Homo sapiens.
XX PN US2003044417-A1.
XX PD 06-MAR-2003.
XX PP 31-MAR-2000; 2000US-00539382.
XX PR 24-SEP-1999; 99US-0155979P.
XX PA (MCCO/) MCCORMICK A A.
XX PA (TUSE/) TUSE D.
XX PA (REIN/) REINL S J.
XX PA (LIND/) LINDBO J A.
XX PA (TURP/) TURPEN T H.
XX PI McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
XX WPI; 2003-456551/43.
XX DR P-ESDB; ABO01257.
XX PT Novel polypeptide self-antigen useful as tumor-specific vaccine in
XX PT mammals, is produced in plants and mimics one or more epitopes of antigen
XX PT uniquely expressed by cells of tumor.
XX PS Example 2; Page 23; 37pp; English.
XX CC The invention describes a polypeptide self-antigen (I) useful as a tumour
XX CC -specific vaccine in a subject with a tumour or at risk of developing a
XX CC tumour, encoded by a nucleic acid in the cells of the tumour, including
XX CC an epitope to, or overexpressed by tumour cells; produced in a cell or
XX CC organism that has been transfected with nucleic acid and in a correctly
XX CC folded form; and capable of inducing an immune response in a mammal. (I)
XX CC is useful as a tumour-specific vaccine, especially a B-cell lymphoma-
XX CC specific vaccine. A vaccine composition is useful for inducing a tumour-
XX CC specific immune antibody response in a tumour-bearing subject, preferably
XX CC human or a subject who had a tumour and was treated so that no tumour is
XX CC clinically or radiographically evident, where the tumour is B-cell
XX CC lymphoma. This sequence encodes a linker peptide associated with single
XX CC chain antibody polypeptides which function to join the variable heavy and
XX CC variable light chain encoding DNA's together forming the single chain
XX CC antibody
XX SQ Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTGCTGCTAGT 39
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGCTGCTAGT 39

RESULT 6
ACD45089
ID ACD45089 standard; DNA; 39 BP.
XX AC ACD45089;
XX AC ACD45089;
```


DT 06-AUG-2003 (revised)

DT 11-SEP-2001 (first entry)
XX Shrimp white spot Bacilliform virus (WSBV) genomic sequence.
DE
XX
XX Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW antiviral agent; gene expression; antisense construct;
KW transgenic viral resistant shrimp; ds.
XX
XX Shrimp white spot syndrome virus.
XX
XX W0200138351-A2.
XX
XX 31-MAY-2001.
XX
XX 08-NOV-2000; 2000WO-US028888.
XX
XX 24-NOV-1999; 99CN-00124717.
XX (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
XX
PI Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
XX WPI; 2001-355877/37.
DR
XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PT (WSBV), useful for producing viral polypeptides that can be used to
PT screen for agents that are useful for treating WSBV infection.
XX
PS Disclosure; Fig 2; 626pp; English.
XX
XX The invention provides the primary nucleotide sequence of the WSBV genome
CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
CC encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
CC molecules and subunits of the invention are useful for diagnosis and
CC monitoring viral infection, in screens for antiviral agents and for
CC monitoring viral gene expression or activity during a treatment regimen.
CC The nucleic acid molecules are also useful as antisense constructs to
CC control viral gene expression in infected cells and tissues and to create
CC transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 305107 BP; 92042 A; 62482 C; 62635 G; 87948 T; 0 U; 0 Other;
Query Match 74.4%; Score 29; DB 4; Length 305107;
Best Local Similarity 86.5%; Pred. No. 5.5;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACTACTGCTACTGCTGCTACTGCTACTGCTGCTGCTA 37
DB 44222 ACTGCTGCTACTGCTGCTACTGCTACTGCTGCTGCTA 44186
RESULT 11
ADQ97348/C
ID ADQ97348 standard; DNA; 204803 BP.
XX
XX ADQ97348;
XX
XX 07-OCT-2004 (first entry)
DT
XX Mouse cancer associated sequence MD08-036, SEQ ID 325.
DE
XX Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
KW
XX Mus musculus.
OS
XX W02004060304-A2.
PN
XX 22-JUL-2004.
PD
XX

PF 22-DEC-2003; 2003WO-US041389.
XX
XX 27-DEC-2002; 2002US-00330773.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Malandro MS;
PI WPI; 2004-543781/52.
XX
XX New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX
XX Claim 1; SEQ ID NO 325; 199pp; English.
XX
XX The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 204803 BP; 55167 A; 44951 C; 46757 G; 55510 T; 0 U; 2418 Other;
Query Match 73.3%; Score 28.6; DB 12; Length 204803;
Best Local Similarity 88.6%; Pred. No. 7.2;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CTACTGCTACTGCTGCTACTGCTACTGCTGCTGCT 36
DB 92554 CTACTGCTACTGCTGCTACTGCTACTGCTGCTGCT 92520
RESULT 12
AAH20262
ID AAH20262 standard; DNA; 39 BP.
XX
XX AAH20262;
AC
XX 27-JUL-2001 (first entry)
DT
XX CJ linker library oligonucleotide sequence SEQ ID 16.
DE
XX Polynucleotide library; dual-domain; linker; vaccine; B-cell lymphoma;
KW ds.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT CDS 1..39
FT /*tag= a
FT /partial
FT /product= "Linker"
FT /note= "No stop or start codon given"
XX
XX W0200123543-A1.
XX
XX 05-APR-2001.
PD
XX 22-SEP-2000; 2000WO-US025965.
PF
XX 24-SEP-1999; 99US-0155978P.
PR
XX (LARG-) LARGE SCALE BIOLOGY CORP.
PA
XX Reinl SJ, Lindbo JA, Turpen T;
XX WPI; 2001-316135/33.
DR P-PSDB; AAB97231.
DR
XX Novel library of dual-domain nucleic acid molecules useful for producing
PT dual-domain proteins, or idiotypic scFv vaccine useful for treating B-

SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 72.8%; Score 28.4; DB 8; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CTACTGCTACTGGTGTAGTACTGCTGCTGCTGCTAGT 39
||||| | | | | | | | | | | | | | | | | | | |
Db 2 CTACTGCTAGTACTGCTGCTGCTGCTGCTGCTAGT 39
||||| | | | | | | | | | | | | | | | | | | |
Search completed: July 30, 2005, 07:14:49
Job time : 276 secs

RESULT 15
ACD06881
ID ACD06881 standard; DNA; 39 BP.
XX AC ACD06881;
XX AC ACD06881;
DT 06-AUG-2003 (first entry)
XX Immunogenic single chain antibody polypeptide (scfv) linker DNA #3.
XX Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine;
KW self-antigen; tumour-specific vaccine; B-cell lymphoma-specific vaccine;
KW B-cell lymphoma; single chain antibody polypeptide; scfv; ds.
XX Homo sapiens.
OS
XX
XX US2003044420-A1.
PN
XX 06-MAR-2003.
PD
XX
XX 08-FEB-2002; 2002US-00067893.
PF
XX 24-SEP-1999; 99US-0155979P.
PR
XX 10-MAR-2000; 2000US-00522900.
PR
XX (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
PA (REIN/) REINL S J.
PA (LIND/) LINDBO J A.
PA (TURP/) TURPEN T H.
XX McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
PI MPI; 2003-456552/43.
XX
XX Novel polypeptide self-antigen useful as tumor-specific vaccine in
PT mammals, is produced in plants and mimics one or more epitopes of antigen
PT uniquely expressed by cells of tumor.
PT
XX
XX Example 2; Page 21; 47pp; English.
XX
XX The invention describes a polypeptide self-antigen (I) useful as a tumour
CC -specific vaccine in a subject with a tumour or at risk of developing a
CC tumour, encoded by a nucleic acid (NA) in the cells of the tumour,
CC including an epitope to, or overexpressed by tumour cells; produced in a
CC cell or organism that has been transfected with NA and in a correctly
CC folded form; and capable of inducing an immune response in a mammal. (I)
CC is useful as a tumour-specific vaccine, especially a B-cell lymphoma-
CC specific vaccine. A vaccine is useful for inducing a tumour-specific
CC immune antibody response in a tumour-bearing subject, preferably human or
CC a subject who had a tumour and was treated so that no tumour is
CC clinically or radiographically evident, where the tumour is B-cell
CC lymphoma. This sequence encodes a linker peptide that joins a variable
CC heavy chain region to a variable light chain region to form a single
CC chain antibody polypeptide useful in the tumour-specific vaccine of the
CC invention
XX
SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 72.8%; Score 28.4; DB 9; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 07:02:14 ; Search time 97 Seconds
(without alignments)
657.884 Million cell updates/sec

Title: US-09-667-237B-12

Perfect score: 39

Sequence: 1 actactgctactggtgtagtactactgctggtgtagt 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27.8	71.3	3376	1	US-08-320-559-29 Sequence 29, Appl
C 2	27.8	71.3	3376	3	US-08-545-860D-29 Sequence 29, Appl
C 3	27.8	71.3	3376	5	PCT-US94-04496-29 Sequence 29, Appl
C 4	26.8	68.7	1534	1	US-07-973-431B-2 Sequence 2, Appl
C 5	26.4	67.7	1037	4	US-09-181-585-3 Sequence 3, Appl
C 6	26.4	67.7	1159	4	US-09-181-585-1 Sequence 1, Appl
C 7	26.4	67.7	1471	4	US-09-181-585-2 Sequence 2, Appl
C 8	26.2	67.2	601	4	US-09-949-016-189405 Sequence 189405, Appl
C 9	26.2	67.2	601	4	US-09-949-016-189406 Sequence 189406, Appl
C 10	26.2	67.2	601	4	US-09-949-016-189407 Sequence 189407, Appl
C 11	26.2	67.2	601	4	US-09-949-016-189408 Sequence 189408, Appl
C 12	26.2	67.2	601	4	US-09-949-016-189409 Sequence 189409, Appl
C 13	26.2	67.2	825	4	US-09-248-796A-7819 Sequence 7819, Appl
C 14	26.2	67.2	92074	4	US-09-949-016-17163 Sequence 17163, A
C 15	26.2	67.2	678533	4	US-09-949-016-14577 Sequence 14577, A
C 16	26.2	67.2	678533	4	US-09-949-016-14578 Sequence 14578, A
C 17	26	66.7	1449	4	US-09-614-221A-468 Sequence 468, Appl
C 18	25.2	64.6	939	4	US-09-248-796A-6040 Sequence 6040, Appl
C 19	24.8	63.6	1830	4	US-09-248-796A-409 Sequence 409, Appl
C 20	24.6	63.1	420	4	US-09-248-796A-1859 Sequence 1859, Appl
C 21	24.6	63.1	517	4	US-09-640-211A-1352 Sequence 1352, Appl
C 22	24.6	63.1	601	4	US-09-949-016-93964 Sequence 93964, A
C 23	24.6	63.1	648	4	US-09-248-796A-8852 Sequence 8852, Appl
C 24	24.6	63.1	1188	4	US-09-362-842-5 Sequence 5, Appl
C 25	24.6	63.1	1671	4	US-09-248-796A-8235 Sequence 8235, Appl
C 26	24.6	63.1	2289	4	US-09-248-796A-5548 Sequence 5548, Appl
C 27	24.6	63.1	2369	3	US-08-910-925-2 Sequence 2, Appl

C 28	24.6	63.1	2617	4	US-09-949-016-1390 Sequence 390, App
C 29	24.6	63.1	9879	4	US-09-949-016-13270 Sequence 13270, A
C 30	24.6	63.1	12921	4	US-09-949-016-14446 Sequence 14446, A
C 31	24.6	63.1	26587	4	US-09-949-016-16636 Sequence 16636, A
C 32	24.6	63.1	83428	4	US-09-949-016-13610 Sequence 13610, A
C 33	24.6	63.1	108169	4	US-09-949-016-12898 Sequence 12898, A
C 34	24.6	63.1	108169	4	US-09-949-016-15907 Sequence 15907, A
C 35	24.6	63.1	140925	4	US-09-949-016-11777 Sequence 11777, A
C 36	24.6	63.1	140982	4	US-09-949-016-16295 Sequence 16295, A
C 37	24.6	63.1	301828	4	US-09-949-016-13969 Sequence 13969, A
C 38	24.4	62.6	393	4	US-09-248-796A-2714 Sequence 2714, Ap
C 39	24.4	62.6	609	4	US-09-248-796A-3807 Sequence 3807, Ap
C 40	24.4	62.6	1266	4	US-09-248-796A-314 Sequence 314, App
C 41	24.2	62.1	246	4	US-09-248-796A-6639 Sequence 6639, Ap
C 42	24.2	62.1	601	4	US-09-949-016-93963 Sequence 93963, A
C 43	24.2	62.1	615	4	US-09-248-796A-2859 Sequence 2859, App
C 44	24.2	62.1	711	4	US-09-248-796A-265 Sequence 265, App
C 45	24.2	62.1	852	4	US-09-248-796A-5507 Sequence 5507, Ap

ALIGNMENTS

RESULT 1

US-08-320-559-29/c

; Sequence 29, Application US/08320559

; Patent No. 5633135

; GENERAL INFORMATION:

; APPLICANT: Croce, Carlo

; APPLICANT: Canaani, Eli

; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for

; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias

; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the

; TITLE OF INVENTION: All-1 Region

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION NUMBER: US/08/320,559

; APPLICATION DATE:

; FILING DATE: 435

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/062,443

; FILING DATE: 14 MAY 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/971,094

; FILING DATE: 30-OCT-92

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/888,830

; FILING DATE: 27-MAY-92

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/805,093

; FILING DATE: 11-DEC-91

; ATTORNEY/AGENT INFORMATION:

; NAME: DeLuca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TCU-0855

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3376 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-320-559-29

Query Match          71.3%; Score 27.8; DB 1; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTACTACTACTACTGCTGCTGCTAGT 39
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Db 765 ACTACTGCTGCTGCTGCTGCTACTGCTGCTGCTACT 727

RESULT 2
US-08-545-860D-29/c
; Sequence 29, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140 is
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
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; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-545-860D-29

Query Match          71.3%; Score 27.8; DB 3; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGCTGCTAGT 39
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Db 765 ACTACTGCTGCTGCTGCTGCTACTGCTGCTGCTACT 727

RESULT 3
PCT-US94-04496-29/c
; Sequence 29, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
PCT-US94-04496-29

Query Match          71.3%; Score 27.8; DB 5; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1.6;
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Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTCTACT 39
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Db 765 ACTACTGCTGCTGCTGCTGCTACTGCTGCTACT 727
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RESULT 4
US-07-973-431B-2/c
; Sequence 2, Application US/07973431B
; Patent No. 652144
; GENERAL INFORMATION:
; APPLICANT: Lu, Yinchun
; APPLICANT: Haseltine, William A
; TITLE OF INVENTION: YCI Protein, Gene, And Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; Dike, Bronstein,
; ADDRESSEE: Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,431B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41968
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-07-973-431B-2

Query Match 68.7%; Score 26.8; DB 1; Length 1534;
Best Local Similarity 81.6%; Pred. No. 3.1;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTCTAG 38
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Db 221 ACTGCTGCTACTGTTGTTATTACTGCTGGTGGTCTG 184
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RESULT 5
US-09-181-585-3
; Sequence 3, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181.585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1037

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
; OTHER INFORMATION: comprising exons E, C, and A
US-09-181-585-3

Query Match 67.7%; Score 26.4; DB 4; Length 1037;
Best Local Similarity 83.3%; Pred. No. 4;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 667 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCT 702
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RESULT 6
US-09-181-585-1
; Sequence 1, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181.585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-181-585-1

Query Match 67.7%; Score 26.4; DB 4; Length 1159;
Best Local Similarity 83.3%; Pred. No. 4.1;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTCT 36
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Db 479 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCT 514
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RESULT 7
US-09-181-585-2
; Sequence 2, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181.585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
; OTHER INFORMATION: comprising exons D, C, B, and A
US-09-181-585-2

Query Match 67.7%; Score 26.4; DB 4; Length 1471;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTCT 36
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Db 1101 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCT 1136
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 189409
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189409

Query Match 67.2% Score 26.2; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTACTACTACTGCTGGTGTAGT 39
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Db 397 ACTACTACTATTGCTACTACTACTACTGCTACTACT 359

RESULT 13
US-09-248-796A-7819
; Sequence 7819, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7819
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-7819

Query Match 67.2% Score 26.2; DB 4; Length 825;
Best Local Similarity 79.5%; Pred. No. 4.6;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTACTACTACTGCTGGTGTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 ACTACTGCTACTGCTGCTACTACTGCTACTGCTACT 459

RESULT 14
US-09-949-016-17163
; Sequence 17163, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17163
; LENGTH: 92074
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17163

Query Match          67.2%; Score 26.2; DB 4; Length 92074;
Best Local Similarity 79.5%; Pred. No. 9;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTCTACTACTACTGCTGGTGGCTAGT 39
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Db 40991 ACTACTACTATTGTCTACTACTACTACTGCTACTACT 41029

RESULT 15
US-09-949-016-14577/c
; Sequence 14577, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14577
; LENGTH: 678533
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(678533)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14577

Query Match          67.2%; Score 26.2; DB 4; Length 678533;
Best Local Similarity 79.5%; Pred. No. 12;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTCTACTACTACTGCTGGTGGCTAGT 39
      ||||| ||||| ||||| ||||| ||||| |||||
Db 216377 ACTACTACTACTACTACTACTACTACTGCTAGTAGT 216339

Search completed: July 30, 2005, 08:17:06
Job time : 101 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 07:10:14 ; Search time 412 Seconds
(without alignments)
612.675 Million cell updates/sec

Title: US-09-667-237B-12
Perfect score: 39
Sequence: 1 actactgctactgtagtagtactactgctggtgtagt 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	39	10	US-09-539-382-45
2	39	100.0	39	14	US-10-067-790-45
3	39	100.0	39	14	US-10-067-892-45
4	39	100.0	39	14	US-10-067-893-45
5	30	76.9	109453	19	US-10-388-838-81
6	29.4	75.4	192	19	US-10-674-124A-10191
7	29	74.4	201	20	US-10-719-993-1896
					Sequence 10191, A
					Sequence 1896, Ap

c 8	29	74.4	201	20	US-10-719-993-1903	Sequence 1903, Ap
c 9	29	74.4	201	20	US-10-719-993-1907	Sequence 1907, Ap
c 10	29	74.4	201	20	US-10-719-993-10972	Sequence 10972, A
c 11	29	74.4	2059	17	US-10-442-017-16	Sequence 16, Appl
c 12	29	74.4	3179	20	US-10-719-993-97	Sequence 97, Appl
c 13	29	74.4	3261	20	US-10-719-993-95	Sequence 95, Appl
c 14	29	74.4	3637	20	US-10-719-993-96	Sequence 96, Appl
c 15	29	74.4	289730	20	US-10-719-993-6780	Sequence 6780, Ap
	28.4	72.8	39	10	US-09-539-382-49	Sequence 49, Appl
	28.4	72.8	39	14	US-10-067-790-49	Sequence 49, Appl
	28.4	72.8	39	14	US-10-067-893-49	Sequence 49, Appl
	28.4	72.8	39	14	US-10-067-892-49	Sequence 49, Appl
c 20	27.8	71.3	201	20	US-10-719-993-1895	Sequence 1895, Ap
c 21	27.8	71.3	201	20	US-10-719-993-1902	Sequence 1902, Ap
c 22	27.8	71.3	201	20	US-10-719-993-1906	Sequence 1906, Ap
c 23	27.8	71.3	201	20	US-10-719-993-10948	Sequence 10948, A
c 24	27.8	71.3	488	10	US-09-918-995-19918	Sequence 19918, A
c 25	27.8	71.3	495	21	US-10-800-322-55	Sequence 55, Appl
c 26	27.8	71.3	544	16	US-10-029-386-22806	Sequence 22806, A
c 27	27.8	71.3	553	9	US-09-920-300A-1461	Sequence 1461, Ap
c 28	27.8	71.3	553	13	US-10-033-528-1461	Sequence 1461, Ap
c 29	27.8	71.3	553	16	US-10-099-926-1461	Sequence 1461, Ap
c 30	27.8	71.3	553	22	US-10-961-527-1461	Sequence 1461, Ap
c 31	27.8	71.3	586	16	US-10-029-386-9094	Sequence 9094, Ap
c 32	27	69.2	2510	17	US-10-172-118-1031	Sequence 1031, Ap
c 33	27	69.2	2510	18	US-10-342-887-1031	Sequence 1031, Ap
c 34	27	69.2	3277	20	US-10-723-860-463	Sequence 463, App
c 35	26.8	68.7	60	10	US-09-539-382-55	Sequence 55, Appl
c 36	26.8	68.7	60	14	US-10-067-790-55	Sequence 55, Appl
c 37	26.8	68.7	60	14	US-10-067-892-55	Sequence 55, Appl
c 38	26.8	68.7	60	14	US-10-067-893-55	Sequence 55, Appl
c 39	26.8	68.7	1369	19	US-10-322-281-28	Sequence 28, Appl
c 40	26.8	68.7	1500	16	US-10-369-909-67	Sequence 67, Appl
c 41	26.8	68.7	1509	14	US-10-175-523-40	Sequence 40, Appl
c 42	26.8	68.7	1536	21	US-10-965-898-90	Sequence 90, Appl
c 43	26.8	68.7	1679	17	US-10-172-118-1675	Sequence 1675, Ap
c 44	26.8	68.7	1679	18	US-10-342-887-1675	Sequence 1675, Ap
c 45	26.8	68.7	88232	13	US-10-087-192-1699	Sequence 1699, Ap

ALIGNMENTS

RESULT 1
US-09-539-382-45
; Sequence 45, Application US/09539382
; Publication No. US2003004417A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CANCERS
; FILE REFERENCE: 18696-169195
; CURRENT APPLICATION NUMBER: US/09/539,382
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: linker
US-09-539-382-45

Query Match 100.0%; Score 39; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||

RESULT 2

US-10-067-790-45
; Sequence 45, Application US/10067790
; Publication No. US20030035807A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,790
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/522,900
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: linker
US-10-067-790-45

Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||

RESULT 3

US-10-067-892-45
; Sequence 45, Application US/10067892
; Publication No. US20030039659A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,892
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/522,900
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: linker

US-10-067-892-45

Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||

RESULT 4

US-10-067-893-45
; Sequence 45, Application US/10067893
; Publication No. US2003004420A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,893
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 09/522,900
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: linker
US-10-067-893-45

Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||

RESULT 5

US-10-388-838-81
; Sequence 81, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 109453
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-388-838-81

Query Match 76.9%; Score 30; DB 19; Length 109453;
Best Local Similarity 86.8%; Pred. No. 1.4;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CTACTGCTAGTCTAGTACTACTGCTGCTAGT 39
Db 22948 CTGCTGCTGCTGGTGGTAGTATTCCTGCTGCTGCTAGT 22985

RESULT 6

US-10-674-124A-10191/c
; Sequence 10191, Application US/10674124A
; Publication No. US2004019797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 10191
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DIS07_10002156
; FEATURE:
; OTHER INFORMATION: Located on chromosome 6
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: 5'-terminus of this base sequence : 140955
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 140955
US-10-674-124A-10191

Query Match 75.4%; Score 29.4; DB 19; Length 192;
Best Local Similarity 84.6%; Pred. No. 0.8;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTAGTCTGCTAGTACTACTGCTGCTGCTAGT 39
Db 132 ACTACTGCTGCTGCTAGTACTACTACTGCTGCTATT 94

RESULT 7

US-10-719-993-1896/c
; Sequence 1896, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1896
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
US-10-719-993-1896

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTAGTCTGCTAGTACTACTGCTGCTGCTAGT 39
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 8

US-10-719-993-1903/c
; Sequence 1903, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1903
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
US-10-719-993-1903

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTAGTCTGCTAGTACTACTGCTGCTGCTAGT 39
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 9

US-10-719-993-1907/c
; Sequence 1907, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1907
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
US-10-719-993-1907

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTAGTCTGCTAGTACTACTGCTGCTGCTAGT 39
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 10

US-10-719-993-10972/c
; Sequence 10972, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
US-10-719-993-10972

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; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10972
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-10972

Query Match      74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 ACTACTGCTGCTGCTGCTCTACTGCTGCTGCTACT 84
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-442-017-16/c
; Sequence 16, Application US/10442017
; Publication No. US20030215950A1
; GENERAL INFORMATION:
; APPLICANT: Battelle Memorial Institute
; APPLICANT: LaSalle, Linda L.
; APPLICANT: Dai, Ziyu
; TITLE OF INVENTION: Isolated Polynucleotides and Methods of Promoting a Morphology In
; FILE REFERENCE: BA4-195
; CURRENT APPLICATION NUMBER: US/10/442,017
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/382,132
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 2059
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-442-017-16

Query Match      74.4%; Score 29; DB 17; Length 2059;
Best Local Similarity 86.5%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1396 TGCTGCTGCTAGTCTAGTCTAGTCTGCTGCTAGT 1360
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-10-719-993-97/c
; Sequence 97, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 3179
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-97

Query Match      74.4%; Score 29; DB 20; Length 3179;
```

```
Best Local Similarity 82.1%; Pred. No. 1.7;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 ACTACTGCTGCTGCTGCTCTCTACTGCTGCTGCTACT 825
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-10-719-993-95/c
; Sequence 95, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-95

Query Match      74.4%; Score 29; DB 20; Length 3261;
Best Local Similarity 82.1%; Pred. No. 1.7;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 ACTACTGCTGCTGCTGCTCTCTACTGCTGCTGCTACT 825
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-719-993-96/c
; Sequence 96, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-96

Query Match      74.4%; Score 29; DB 20; Length 3637;
Best Local Similarity 82.1%; Pred. No. 1.8;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 ACTACTGCTGCTGCTGCTCTCTACTGCTGCTGCTACT 825
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-10-719-993-6780/c
; Sequence 6780, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 3179
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-97

Query Match      74.4%; Score 29; DB 20; Length 3179;
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; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6780
; LENGTH: 289730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(289730)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6780

Query Match      74.4%; Score 29; DB 20; Length 289730;
Best Local Similarity 82.1%; Pred. No. 3.6;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 ACTACTGCTACTGCTGCTAGTACTACTGCTGCTGCTAGT 39
        ||||| ||||| ||||| :||| ||||| |||||
Db      214259 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 214221

Search completed: July 30, 2005, 08:24:04
Job time : 416 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 06:59:54 ; Search time 2067 Seconds
(without alignments)
718.194 Million cell updates/sec

Title: US-09-667-237B-12

Perfect score: 39

Sequence: 1 actactgctactggtctagctactactctgctggtgtagt 39

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 69479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	33.8	86.7	410	9	FR0021942
C 2	31	79.5	513	8	BZ423698
C 3	31	79.5	619	9	FR0006944
C 4	30.6	78.5	280	9	FR0019522
C 5	30	76.9	152	9	FR0013693
C 6	30	76.9	480	8	BZ643398
C 7	30	76.9	493	1	AL931932
C 8	30	76.9	843	8	BZ643413
C 9	29.4	75.4	207	9	FR0021848
C 10	29.4	75.4	257	9	FR0026883
C 11	29.4	75.4	307	8	BZ683794
C 12	29.4	75.4	470	9	FR0018463
C 13	29.4	75.4	472	8	AQ934726
C 14	29.4	75.4	526	9	CNS03CM0
C 15	29.4	75.4	735	9	CNS04NSM
C 16	29.4	75.4	764	9	CG290979
C 17	29.4	75.4	951	9	CNS0414A
C 18	29	74.4	940	8	AZ205951
C 19	28.6	73.3	425	9	CNS01XJ9
C 20	28.6	73.3	469	9	FL569187
C 21	28.6	73.3	610	9	FR0047551
C 22	28.4	72.8	262	9	CE385582
C 23	28.4	72.8	452	2	BE679837
C 24	28.4	72.8	477	9	FR0026865

C 25	28.4	72.8	500	5	BP190034
C 26	28.4	72.8	567	9	PR0006951
C 27	28.4	72.8	619	9	FR0047423
C 28	28.4	72.8	661	4	BJ661564
C 29	28.4	72.8	676	4	BJ649626
C 30	28.4	72.8	805	9	CNS04RW2
C 31	28.4	72.8	818	9	CL843342
C 32	28.4	72.8	905	9	CL288114
C 33	28.4	72.8	939	9	CG900918
C 34	28.4	72.8	993	8	AQ687985
C 35	28	71.8	168	8	BH784725
C 36	28	71.8	267	9	CE589218
C 37	28	71.8	388	9	FR0019523
C 38	28	71.8	548	7	CN251992
C 39	28	71.8	562	5	BUI26074
C 40	28	71.8	580	8	BH763893
C 41	28	71.8	659	4	BM627819
C 42	28	71.8	684	2	BF612474
C 43	28	71.8	687	5	BUI26727
C 44	28	71.8	689	5	BUI26090
C 45	28	71.8	690	2	BF612625

ALIGNMENTS

RESULT 1
LOCUS FR0021942/c 410 bp DNA linear GSS 25-FEB-2004
DEFINITION F.rubripes GSS sequence, clone 070F18AB11, genomic survey sequence.
ACCESSION AL014813
VERSION AL014813.1 GI:2681181
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.
REFERENCE 1
AUTHORS Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J., Bouchireb, N., Cottage, A., Yeo, G.S., Umrانيا, Y., Williams, G. and Brenner, S.
TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning
JOURNAL Genome Res. 9 (10), 960-971 (1999)
MEDLINE 99455097
PubMed 10523524
REFERENCE 2 (bases 1 to 410)
AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrانيا, Y., Williams, G. and Brenner, S.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgm.mrc.ac.uk
COMMENT Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic sequence.
FEATURES
source Location/Qualifiers
1. 410
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="070F18AB11"
/clone_lib="cosmid 070F18"

ORIGIN
Query Match 86.7%; Score 33.8; DB 9; Length 410;
Best Local Similarity 89.7%; Pred. No. 0.078; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 4;


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    Plate: P87 row: E column: 03.
    Location/Qualifiers
      1..493
        /organism="Anopheles gambiae"
        /mol_type="mRNA"
        /db_xref="taxon:7165"
        /clone="NAP1-P87-E-03-5"
        /lab_host="E. coli DH10B"
        /clone_lib="NAP1"
        /note="Vector: pT73D-Pac (Pharmacia); Site 1: NotI;
        Site 2: EcoRI; ESTs sequenced from the T7 priming site
        that reads from the 5' end of cDNA. The NAP1 is a
        directionally cloned and normalized, oligo-T primed cDNA
        library constructed from a mixture of Anopheles gambiae
        developmental stages according to: Bonaldo, Lennon &
        Soares (1996): Normalization and Subtraction: Two
        Approaches To Facilitate Gene Discovery, Genome Research
        6, 791-806."

ORIGIN
  Query Match      76.9%; Score 30; DB 1; Length 493;
  Best Local Similarity 86.8%; Pred. No. 1.8;
  Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGCTGCTAG 38
Db 305 ACTACTGCTGCTGCTGCTAGTACTACTGCTGCTAG 268

RESULT 8
BZ643413/c
LOCUS
DEFINITION
  OGAOW577M ZM 0.7 1.5 KB Zea mays genomic clone ZMBMa011J17,
  genomic survey sequence.
VERSION
  BZ643413
KEYWORDS
  BZ643413.1 GI:28104915
SOURCE
  Zea mays
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 843)
    WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
    Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
    Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
    Consortium for Maize Genomics
    Unpublished (2002)
  Other_GSSs: OGAOW57TC
  Contact: Cathy WhiteIaw
  TIGR
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301-838-5843
    Fax: 301-838-0208
    Email: whiteIaw@tigr.org
  Seq primer: TR
  Class: sheared ends.

FEATURES
  source
    Location/Qualifiers
      1..843
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        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
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  Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CTACTGCTACTGCTGCTAGTACTACTGCTGCTGCTAGT 39
Db 458 CTACTGCTACTGCTACTACTACTACTGCTGCTGCTACT 421

RESULT 9
FR0021848/c
LOCUS
DEFINITION
  F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.
ACCESSION
  AL014719
VERSION
  AL014719.1 GI:2681087
KEYWORDS
  GSS; genome survey sequence.
SOURCE
  Takifugu rubripes (Fugu rubripes)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
    Tetraodontoidea; Tetraodontidae; Takifugu.
  1
    Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
    Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and
    Brenner,S.
    Generation and analysis of 25 Mb of genomic DNA from the pufferfish
    Fugu rubripes by sequence scanning
    Genome Res. 9 (10), 960-971 (1999)
    99455097
    PUBMED
    10523524
  REFERENCE
    2 (bases 1 to 207)
    Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
    Williams,G. and Brenner,S.
    Direct Submission
    Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
    Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk
    Vector: pBluescript II KS
    V type: phagemid
    PRIMER: KS
    DESCR:
      One pass dye-terminator sequencing of cosmid cloned genomic
      sequence.
  FEATURES
    source
      Location/Qualifiers
        1..207
          /organism="Takifugu rubripes"
          /mol_type="genomic DNA"
          /db_xref="taxon:31033"
          /clone="069K22aG2"
          /clone_lib="cosmid 069K22"

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  Best Local Similarity 84.6%; Pred. No. 2.8;
  Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGCTGCTAGT 39
Db 102 ACTGCTGCTACTGCTGCTACTACTGCTGCTGCTGCTACT 64

RESULT 10
FR0026883
LOCUS
DEFINITION
  F.rubripes GSS sequence, clone 181A15aD3, genomic survey sequence.
ACCESSION
  AL019712
VERSION
  AL019712.1 GI:2686080
KEYWORDS
  GSS; genome survey sequence.
SOURCE
  Takifugu rubripes (Fugu rubripes)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
    Tetraodontoidea; Tetraodontidae; Takifugu.
  1
    Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
    Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and
    Brenner,S.
    Generation and analysis of 25 Mb of genomic DNA from the pufferfish
    Fugu rubripes by sequence scanning
    Genome Res. 9 (10), 960-971 (1999)
    99455097
    PUBMED
    10523524
  REFERENCE
    2 (bases 1 to 207)
    Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
    Williams,G. and Brenner,S.
    Direct Submission
    Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
    Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk
    Vector: pBluescript II KS
    V type: phagemid
    PRIMER: KS
    DESCR:
      One pass dye-terminator sequencing of cosmid cloned genomic
      sequence.
  FEATURES
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        1..207
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Brenner,S.
Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
MEDLINE PUBMED 99455097
REFERENCE 10523524
2 (bases 1 to 257)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.mrc.ac.uk
Vector: pBluescript II KS
V.type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
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                /db_xref="taxon:31033"
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Best Local Similarity 84.6%; Pred. No. 2.8;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGCTAGTACTACTGCTGCTGCTAGT 39
Db 155 ACTACTGCTACTGCTAGTACTACTGCTGCTGCTACT 193

RESULT 11
BZ683794/c
LOCUS BZ683794 307 bp DNA linear GSS 05-FEB-2003
DEFINITION PUBCV45TD ZM 0.6-1.0 KB Zea mays genomic clone ZMMBTa026G18,
genomic survey sequence.
ACCESSION BZ683794
VERSION BZ683794.1 GI:28241439
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 307)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: Tp
Class: Sheared ends.
FEATURES
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            1..307
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                /mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 84.6%; Pred. No. 2.9;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGCTAGTACTACTGCTGCTGCTAGT 39
Db 155 ACTGCTGCTACTACTGCTACTACTACTGCTGCTGCTACT 117

RESULT 12
FR0018463/c
LOCUS FR0018463 470 bp DNA linear GSS 25-FEB-2004
DEFINITION F. rubripes GSS sequence, clone 016E10aC6, genomic survey sequence.
ACCESSION AL011359
VERSION AL011359.1 GI:2676793
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Takifugu.
1
Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and
Brenner,S.
Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
99455097
10523524
2 (bases 1 to 470)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.mrc.ac.uk
Vector: pBluescript II KS
V.type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
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Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGCTAGTACTACTGCTGCTGCTAGT 39
Db 303 ACTACTGCTACTGCTAGTACTACTGCTGCTGCTACT 265

RESULT 13
AQ934726
LOCUS AQ934726 472 bp DNA linear GSS 21-DEC-1999
DEFINITION RPCI-23-290D23-TV RPCI-23 Mus musculus genomic clone
RPCI-23-290D23, genomic survey sequence.
ACCESSION AQ934726
VERSION AQ934726.1 GI:6623740
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 735)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
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/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="123M05"
/clone_lib="G"
/note="Genoscope sequence ID : C08G123AG03LP1-end : T7"
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Best Local Similarity 84.6%; Pred. No. 3.1;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGCTGCTACTACTGCTGCTGCTAGT 39
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Db 451 ACTACTACTACTGCTACTGCTACTGCTGCTGCTACT 413

Search completed: July 30, 2005, 08:15:25
Job time : 2074 secs

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Reini,S.J., Lindbo,J.A. and Turpen,T.
TITLE        Creation of variable length and sequence linker regions for
              dual-domain or multi-domain molecules
JOURNAL      Patent: WO 0123543-A 12 05-APR-2001;
              Large Scale Biology Corporation (US)
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    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="linker region nucleotide sequence"
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Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    |||||
Db 2 TACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 38
    |||||
RESULT 3
AP006490 7/c
WPCOMMENT
Sequence split into 8 fragments LOCUS AP006490 Accession AP006490
Fragment Name      Begin      End
- AP006490.0       100001    210000
- AP006490.1       200001    310000
- AP006490.2       300001    410000
- AP006490.3       400001    510000
- AP006490.4       500001    610000
- AP006490.5       600001    710000
- AP006490.6       700001    740346
Continuation (8 of 8) of AP006490 from base 700001 (AP006490 Cyanidioschyzon merolae str
Query Match      81.0%; Score 31.6; DB 2; Length 40346;
Best Local Similarity 89.5%; Pred. No. 1.4;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    |||||
Db 4932 CTACTGCTACTGGTCTAGTACTGCTATTGCTAGTCTACT 4895
    |||||
RESULT 4
AP006490 6/c
WPCOMMENT
Sequence split into 8 fragments LOCUS AP006490 Accession AP006490
Fragment Name      Begin      End
- AP006490.0       100001    210000
- AP006490.1       200001    310000
- AP006490.2       300001    410000
- AP006490.3       400001    510000
- AP006490.4       500001    610000
- AP006490.5       600001    710000
- AP006490.6       700001    740346
Continuation (7 of 8) of AP006490 from base 600001 (AP006490 Cyanidioschyzon merolae str
Query Match      81.0%; Score 31.6; DB 2; Length 110000;
Best Local Similarity 89.5%; Pred. No. 1.3;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
    |||||
Db 104932 CTACTGCTACTGGTCTAGTACTGCTATTGCTAGTCTAGT 104895
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RESULT 5
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BX004814/c
LOCUS
DEFINITION
  Zebrafish DNA sequence from clone CH211-10316 in linkage group 1,
  complete sequence.
ACCESSION
  BX004814
VERSION
  BX004814.8 GI:39540497
KEYWORDS
  HTG.
SOURCE
  Danio rerio (zebrafish)
ORGANISM
  Danio rerio
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
  1 (bases 1 to 171710)
  Howden,P.
  Direct Submission
  Submitted (06-DEC-2003) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  zfsh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
  On Dec 6, 2003 this sequence version replaced gi:31620701.
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: zfsh-help@sanger.ac.uk
  -----
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest, except on the rare
  occasion of the clone being a YAC.
  The following abbreviations are used to associate primary accession
  numbers given in the feature table with their source databases:
  Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
  on the WORMPEP database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names
  beginning 'Dr' were identified by the Recon repeat discovery system
  (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr'
  were identified by Rick Waterman (Stephen Johnson lab, WashU). For
  further information see
  http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-10316
  is from a CHORI-211 BAC library
  VECTOR: pTARBAC2.1
  Clone-derived Zebrafish pUC subclones occasionally display
  inconsistency over the length of mononucleotide A/T runs and
  conserved TA repeats. Where this is found the longest good quality
  representation will be submitted.
FEATURES
  Location/Qualifiers
    source
      1..171710
      /organism="Danio rerio"
      /mol_type="genomic DNA"
      /db_xref="taxon:7955"
      /clone="CH211-10316"
      /clone_lib="CHORI-211"
ORIGIN
Query Match      79.5%; Score 31; DB 5; Length 171710;
Best Local Similarity 87.2%; Pred. No. 2;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGCTGCTAGT 39
    |||||
Db 58965 AGTAGTGCTACTGCTGCTAGTACTGCTAGTCTAGTCTAGT 58927
    |||||
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